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(FILE 'HOME' ENTERED AT 15:13:01 ON 12 JAN 2006)

FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH' ENTERED AT 15:13:45 ON 12 JAN
2006

L1 24946 S STOP CODON OR STOP SIGNAL
L2 228 S L1 AND TRANSPOSON
L3 5 S L2 AND END SEQUENCE
L4 125 S (MODIFY OR CHANGE OR ALTER OR MUTATE OR TRUNCATE) AND END SEQ
L5 2 S L4 AND L1
L6 1 DUP REMOVE L5 (1 DUPLICATE REMOVED)
L7 9 S L4 AND TRANSPOSON
L8 3 DUP REMOVE L7 (6 DUPLICATES REMOVED)

=>

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NEWS 5 DEC 14 2006 MeSH terms loaded for MEDLINE file segment of TOXCENTER
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NEWS 7 DEC 21 IPC search and display fields enhanced in CA/CAPLUS with the
IPC reform
NEWS 8 DEC 23 New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
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NEWS EXPRESS JANUARY 03 CURRENT VERSION FOR WINDOWS IS V8.01,
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=> file medline caplus biosis scisearch

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FILE 'SCISEARCH' ENTERED AT 15:13:45 ON 12 JAN 2006

=> s stop codon or stop signal

L1 24946 STOP CODON OR STOP SIGNAL

=> s l1 and transposon

L2 228 L1 AND TRANSPOSON

=> s l2 and end sequence

2 FILES SEARCHED...

L3 5 L2 AND END SEQUENCE

=>

=> d ibib abs 1-5

L3 ANSWER 1 OF 5 MEDLINE on STN

ACCESSION NUMBER: 2003372847 MEDLINE

DOCUMENT NUMBER: PubMed ID: 12907724

TITLE: The bacterial **transposon** Tn7 causes premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi.

AUTHOR: Lo Clive; Adachi Kiichi; Shuster Jeffrey R; Hamer John E; Hamer Lisbeth

CORPORATE SOURCE: Paradigm Genetics, Inc., 108 Alexander Drive, Research Triangle Park, NC 27709, USA.. clivelo@hkucc.hku.hk

SOURCE: Nucleic acids research, (2003 Aug 15) 31 (16) 4822-7. Journal code: 0411011. ISSN: 1362-4962.

PUB. COUNTRY: England: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200401

ENTRY DATE: Entered STN: 20030809

Last Updated on STN: 20040130

Entered Medline: 20040129

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in *Magnaporthe grisea* and *Mycosphaerella graminicola*. Northern analysis showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation. Polyadenylation signals characteristic of eukaryotic genes, preceded by **stop codons** in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi. Similarly, a particular *M.grisea* CBS1 (encoding cystathionine beta-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo study of truncated gene products in filamentous fungi.

L3 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:837288 CAPLUS

DOCUMENT NUMBER: 139:333968

TITLE: Producing deletion derivatives of polypeptides using modified **transposon** with **stop codons** in all three reading frames

INVENTOR(S): Savilahti, Harri; Tieaho, Ville

PATENT ASSIGNEE(S): Finnzymes Oy, Finland

SOURCE: PCT Int. Appl., 37 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003087370	A1	20031023	WO 2003-FI285	20030414
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
FI 2002000746	A	20031019	FI 2002-746	20020418
US 2005208616	A1	20050922	US 2005-511327	20050330
PRIORITY APPLN. INFO.:			FI 2002-746	A 20020418
			WO 2003-FI285	W 20030414

AB The present invention describes an in vitro transposition-based methodol. for generation of deletion derivs. of polypeptides. An artificial **transposon** containing at least partly within its **transposon** ends a modification with translation **stop codons** in three reading frames is provided. In the method, transposition complexes are assembled using the modified **transposon** and essentially random integrations into the target plasmid, containing a polypeptide coding nucleic acid of interest, are recovered as a plasmid pool. Subsequent manipulation steps including restriction enzyme digestions and ligation result in pools of mutant clones from which deletion derivs. of a polypeptide coding nucleic acid of interest and its resp. deletion polypeptides could be produced.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2003:616864 CAPLUS

DOCUMENT NUMBER: 139:318350

TITLE: The bacterial **transposon** Tn7 causes premature polyadenylation of mRNA in eukaryotic organisms: TAGKO mutagenesis in filamentous fungi

AUTHOR(S): Lo, Clive; Adachi, Kiichi; Shuster, Jeffrey R.; Hamer, John E.; Hamer, Lisbeth

CORPORATE SOURCE: Paradigm Genetics, Inc., Research Triangle Park, NC, 27709, USA

SOURCE: Nucleic Acids Research (2003), 31(16), 4822-4827
CODEN: NARHAD; ISSN: 0305-1048

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in filamentous fungi. The effects of **transposon** insertion on the expression of TAGKO alleles were examined in *Magnaporthe grisea* and *Mycosphaerella graminicola*. Northern anal. showed that stable, truncated transcripts were expressed in the TAGKO mutants. Mapping of the 3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end sequences**, regardless of the **transposon** orientation. Polyadenylation signals characteristic of eukaryotic genes, preceded by **stop codons** in all frames, are located in both ends of the bacterial **transposon**. Thus, TAGKO transcripts are prematurely polyadenylated, and truncated proteins are predicted to be translated in the fungal mutants. Depending on the extent of protein truncation, TAGKO mutations in HPD4 (encoding p-hydroxyphenylpyruvate dioxygenase) resulted in tyrosine sensitivity in the two fungi. Similarly, a particular *M.grisea* CBS1 (encoding cystathionine β -synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo study of truncated gene products in filamentous fungi.

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 5 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2003:563096 BIOSIS
DOCUMENT NUMBER: PREV200300564228
TITLE: The bacterial **transposon** Tn7 causes premature
polyadenylation of mRNA in eukaryotic organisms: TAGKO
mutagenesis in filamentous fungi.
AUTHOR(S): Lo, Clive [Reprint Author]; Adachi, Kiichi; Shuster,
Jeffrey R.; Hamer, John E.; Hamer, Lisbeth
CORPORATE SOURCE: Department of Botany, The University of Hong Kong, Pokfulam
Road, Hong Kong, China
clivelo@hkucc.hku.hk
SOURCE: Nucleic Acids Research, (August 15 2003) Vol. 31, No. 16,
pp. 4822-4827. print.
ISSN: 0305-1048 (ISSN print).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Dec 2003
Last Updated on STN: 3 Dec 2003

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis in
filamentous fungi. The effects of **transposon** insertion on the
expression of TAGKO alleles were examined in *Magnaporthe grisea* and
Mycosphaerella graminicola. Northern analysis showed that stable,
truncated transcripts were expressed in the TAGKO mutants. Mapping of the
3'-ends of TAGKO cDNAs revealed that they all contain Tn7 **end**
sequences, regardless of the **transposon** orientation.
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beta-synthase) TAGKO cDNA failed to complement cysteine auxotrophy in a
yeast CBS mutant. TAGKO, therefore, represents a useful tool for in vivo
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L3 ANSWER 5 OF 5 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on
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ACCESSION NUMBER: 2003:724714 SCISEARCH
THE GENUINE ARTICLE: 712DY
TITLE: The bacterial **transposon** Tn7 causes premature
polyadenylation of mRNA in eukaryotic organisms: TAGKO
mutagenesis in filamentous fungi
AUTHOR: Lo C (Reprint); Adachi K; Shuster J R; Hamer J E; Hamer L
CORPORATE SOURCE: Univ Hong Kong, Dept Bot, Pokfulam Rd, Hong Kong, Hong
Kong, Peoples R China (Reprint); Univ Hong Kong, Dept Bot,
Hong Kong, Hong Kong, Peoples R China; Paradigm Genet Inc,
Res Triangle Pk, NC 27709 USA
COUNTRY OF AUTHOR: Peoples R China; USA
SOURCE: NUCLEIC ACIDS RESEARCH, (15 AUG 2003) Vol. 31, No. 16, pp.
4822-4827.
ISSN: 0305-1048.
PUBLISHER: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP,
ENGLAND.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 33
ENTRY DATE: Entered STN: 5 Sep 2003
Last Updated on STN: 5 Sep 2003
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB TAGKO is a Tn7-based transposition system for genome wide mutagenesis
in filamentous fungi. The effects of **transposon** insertion on
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